

LH



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/720,285

DATE: 02/11/2003

TIME: 14:03:51

Input Set : A:\12660-002001.txt

Output Set: N:\CRF4\02112003\I720285.raw

4 <110> APPLICANT: Nomura , Hitoshi
 5 Maeda, Masatsugu
 7 <120> TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEINS
 9 <130> FILE REFERENCE: 12660-002001
 11 <140> CURRENT APPLICATION NUMBER: US 09/720,285
 C--> 12 <141> CURRENT FILING DATE: 2002-09-23
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP99/03351
 15 <151> PRIOR FILING DATE: 1999-06-23
 17 <150> PRIOR APPLICATION NUMBER: JP 10/297409
 18 <151> PRIOR FILING DATE: 1998-10-19
 20 <150> PRIOR APPLICATION NUMBER: JP 10/214720
 21 <151> PRIOR FILING DATE: 1998-06-24
 23 <160> NUMBER OF SEQ ID NOS: 213
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 361
 29 <212> TYPE: PRT
 30 <213> ORGANISM: Homo sapiens
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 35 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
 36 20 25 30
 37 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
 38 35 40 45
 39 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
 40 50 55 60
 41 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
 42 65 70 75 80
 43 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
 44 85 90 95
 45 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
 46 100 105 110
 47 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val
 48 115 120 125
 49 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp
 50 130 135 140
 51 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 52 145 150 155 160
 53 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile
 54 165 170 175
 55 Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys
 56 180 185 190

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ENTERED

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57 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser
58      195      200      205
59 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
60      210      215      220
61 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu
62 225      230      235      240
63 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys
64      245      250      255
65 Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser
66      260      265      270
67 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe
68      275      280      285
69 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly
70      290      295      300
71 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His
72 305      310      315      320
73 Pro Pro Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu
74      325      330      335
75 Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro
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81 <211> LENGTH: 1934

82 <212> TYPE: DNA

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85 <220> FEATURE:

86 <221> NAME/KEY: CDS

87 <222> LOCATION: (441)...(1523)

89 <400> SEQUENCE: 2

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91 gcgtctggcc ctctgcctgc ctctccctga gtgtggctga cagccacgca gctgtgtctg      120
92 tctgtctgcg gcccgatgc cctgctgctg gccgctggt accttccttg ccgtctcttt      180
93 cctctgtctg ctgctctgtg ggacacctgc ctggaggccc agctgcccgt catcagagtg      240
94 acaggtctta tgacagcctg attggtgact cgggctgggt gtggattctc accccaggcc      300
95 tctgcctgct ttctcagacc ctcatctgtc acccccacgc tgaaccacgc tgccaccccc      360
96 agaagcccat cagactgccc ccagcacacg gaatggattt ctgagaaaga agccgaaaca      420
97 gaaggcccggt gggagtcagc atg ccg cgt ggc tgg gcc gcc ccc ttg ctg ctg      473
98      Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu
99      1      5      10
101 ctg ctg ctc cag gga ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc      521
102 Leu Leu Leu Gln Gly Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr
103      15      20      25
105 gat tac ctc cag acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac      569
106 Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His
107      30      35      40
109 ccc agc acg ctc acc ctt acc tgg caa gac cag tat gaa gag ctg aag      617
110 Pro Ser Thr Leu Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys
111      45      50      55

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113	gac	gag	gcc	acc	tcc	tgc	agc	ctc	cac	agg	tcg	gcc	cac	aat	gcc	acg	665
114	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	
115	60					65				70						75	
117	cat	gcc	acc	tac	acc	tgc	cac	atg	gat	gta	ttc	cac	ttc	atg	gcc	gac	713
118	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	
119					80					85					90		
121	gac	att	ttc	agt	gtc	aac	atc	aca	gac	cag	tct	ggc	aac	tac	tcc	cag	761
122	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	
123				95					100					105			
125	gag	tgt	ggc	agc	ttt	ctc	ctg	gct	gag	agc	atc	aag	ccg	gct	ccc	cct	809
126	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	
127			110					115						120			
129	ttc	aac	gtg	act	gtg	acc	ttc	tca	gga	cag	tat	aat	atc	tcc	tgg	cgc	857
130	Phe	Asn	Val	Thr	Val	Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	
131		125					130					135					
133	tca	gat	tac	gaa	gac	cct	gcc	ttc	tac	atg	ctg	aag	ggc	aag	ctt	cag	905
134	Ser	Asp	Tyr	Glu	Asp	Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	
135	140					145					150					155	
137	tat	gag	ctg	cag	tac	agg	aac	cgg	gga	gac	ccc	tgg	gct	gtg	agt	ccg	953
138	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	
139				160						165					170		
141	agg	aga	aag	ctg	atc	tca	gtg	gac	tca	aga	agt	gtc	tcc	ctc	ctc	ccc	1001
142	Arg	Arg	Lys	Leu	Ile	Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	
143				175					180					185			
145	ctg	gag	ttc	cgc	aaa	gac	tcg	agc	tat	gag	ctg	cag	gtg	cgg	gca	ggg	1049
146	Leu	Glu	Phe	Arg	Lys	Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	
147			190					195					200				
149	ccc	atg	cct	ggc	tcc	tcc	tac	cag	ggg	acc	tgg	agt	gaa	tgg	agt	gac	1097
150	Pro	Met	Pro	Gly	Ser	Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	
151		205					210					215					
153	ccg	gtc	atc	ttt	cag	acc	cag	tca	gag	gag	tta	aag	gaa	ggc	tgg	aac	1145
154	Pro	Val	Ile	Phe	Gln	Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	
155	220					225					230					235	
157	cct	cac	ctg	ctg	ctt	ctc	ctc	ctg	ctt	gtc	ata	gtc	ttc	att	cct	gcc	1193
158	Pro	His	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	
159				240						245					250		
161	ttc	tgg	agc	ctg	aag	acc	cat	cca	ttg	tgg	agg	cta	tgg	aag	aag	ata	1241
162	Phe	Trp	Ser	Leu	Lys	Thr	His	Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	
163				255					260					265			
165	tgg	gcc	gtc	ccc	agc	cct	gag	cgg	ttc	ttc	atg	ccc	ctg	tac	aag	ggc	1289
166	Trp	Ala	Val	Pro	Ser	Pro	Glu	Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	
167			270					275					280				
169	tgc	agc	gga	gac	ttc	aag	aaa	tgg	gtg	ggt	gca	ccc	ttc	act	ggc	tcc	1337
170	Cys	Ser	Gly	Asp	Phe	Lys	Lys	Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	
171		285					290					295					
173	agc	ctg	gag	ctg	gga	ccc	tgg	agc	cca	gag	gtg	ccc	tcc	acc	ctg	gag	1385
174	Ser	Leu	Glu	Leu	Gly	Pro	Trp	Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	
175	300					305				310						315	
177	gtg	tac	agc	tgc	cac	cca	ccc	agc	agc	cct	gtg	gag	tgt	gac	ttc	acc	1433

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178 Val Tyr Ser Cys His Pro Pro Ser Ser Pro Val Glu Cys Asp Phe Thr
179                               320                               325                               330
181 agc ccc ggg gac gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg      1481
182 Ser Pro Gly Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val
183                               335                               340                               345
185 gtc att cct ccg cca ctt tcg agc cct gga ccc cag gcc agc      1523
186 Val Ile Pro Pro Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser
187                               350                               355                               360
189 taatgaggct gactggatgt ccagagctgg ccaggccact gggccctgag ccagagacaa      1583
190 ggtcacctgg gctgtgatgt gaagacacct gcagcctttg gtctcctgga tgggcctttg      1643
191 agcctgatgt ttacagtgtc tgttgtgtgtg tgcataatgtg tgttgtgtgca tatgcatgtg      1703
192 tgttgtgtgtg tgtgtcttag gtgcgcagtg gcatgtccac gtgtgtgtga ttgcacgtgc      1763
193 ctgtgggcct gggataatgc ccatggtact ccatgcattc acctgccctg tgcattgtctg      1823
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202 <400> SEQUENCE: 3
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205 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr
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207 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
208 35 40 45
209 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
210 50 55 60
211 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
212 65 70 75 80
213 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
214 85 90 95
215 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
216 100 105 110
217 Leu Leu Ala Glu Ser Lys Ser Glu Lys Ala Asp Leu Ser Gly Leu
218 115 120 125
219 Lys Lys Cys Leu Pro Pro Pro Gly Val Pro Gln Arg Leu Glu Leu
220 130 135 140
222 <210> SEQ ID NO: 4
223 <211> LENGTH: 1779
224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
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228 <221> NAME/KEY: CDS
229 <222> LOCATION: (441)...(872)
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234 tctgtctgcg gccctgcat cctgtctgcg gccgcctggt accttccttg ccgtctcttt      180

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235	cctctgtctg	ctgctctgtg	ggacacctgc	ctggaggccc	agctgcccgt	catcagagt	240
236	acaggtctta	tgacagcctg	attggtgact	cgggctgggt	gtggattctc	accccaggcc	300
237	tctgcctgct	tctcagacc	ctcatctgtc	acccccacgc	tgaaccacgc	tgccaccccc	360
238	agaagcccat	cagactgccc	ccagcacacg	gaatggattt	ctgagaaaaga	agccgaaaca	420
239	gaaggcccgt	gggagtcacg	atg ccg cgt	ggc tgg gcc	gcc ccc ttg	ctc ctg	473
240		Met	Pro	Arg	Gly	Trp	Ala
241		1		5		10	
243	ctg	ctg	ctc	cag	gga	ggc	tgg
244	Leu	Leu	Leu	Gln	Gly	Gly	Trp
245		15		20		25	
247	gat	tac	ctc	cag	acg	gtc	atc
248	Asp	Tyr	Leu	Gln	Thr	Val	Ile
249		30		35		40	
251	ccc	agc	acg	ctc	acc	ctt	acc
252	Pro	Ser	Thr	Leu	Thr	Leu	Thr
253		45		50		55	
255	gac	gag	gcc	acc	tcc	tgc	agc
256	Asp	Glu	Ala	Thr	Ser	Cys	Ser
257	60			65		70	
259	cat	gcc	acc	tac	acc	tgc	cac
260	His	Ala	Thr	Tyr	Thr	Cys	His
261			80			85	
263	gac	att	ttc	agt	gtc	aac	atc
264	Asp	Ile	Phe	Ser	Val	Asn	Ile
265			95			100	
267	gag	tgt	ggc	agc	ttt	ctc	ctg
268	Glu	Cys	Gly	Ser	Phe	Leu	Leu
269			110			115	
271	gat	ctc	agt	gga	ctc	aag	aag
272	Asp	Leu	Ser	Gly	Leu	Lys	Lys
273		125			130		135
275	caa	aga	ctc	gag	cta	tgagctgcag	gtgcgggcag
276	Gln	Arg	Leu	Glu	Leu		
277	140						
279	taccagggga	cctggagtga	atggagtgc	cgggtcatct	ttcagaccca	gtcagaggag	972
280	ttaaaggaag	gctggaaccc	tcacctgctg	cttctcctcc	tgcttgtcat	agtcttcatt	1032
281	cctgccttct	ggagcctgaa	gacccatcca	ttgtggaggc	tatggaagaa	gatatgggcc	1092
282	gtccccagcc	ctgagcgggt	cttcatgccc	ctgtacaagg	gctgcagcgg	agacttcaag	1152
283	aaatgggtgg	gtgcaccctt	cactggctcc	agcctggagc	tgggaccctg	gagccagag	1212
284	gtgccttcca	ccctggaggt	gtacagctgc	cacccaccca	gcagccctgt	ggagtgtgac	1272
285	ttcacagacc	cgggggacga	aggaccccc	cggagctacc	tccgccagt	ggtggctcatt	1332
286	cctccgccac	tttcgagccc	tggaccccag	gccagcta	gaggctgact	ggatgtccag	1392
287	agctggccag	gccactgggc	cctgagccag	agacaaggtc	acctgggctg	tgatgtgaag	1452
288	acacctgcag	ccttttgtct	cctggatggg	cctttgagcc	tgatgtttac	agtgtctgtg	1512
289	tgtgtgtgca	tatgtgtgtg	tgtgcatatg	catgtgtgtg	tgtgtgtgtg	tcttaggtgc	1572
290	gcagtggcat	gtccacgtgt	gtgtgattgc	acgtgcctgt	gggcctggga	taatgccc	1632
291	ggtactccat	gcattcacct	gccctgtgca	tgtctggact	cacggagctc	acccatgtgc	1692
292	acaagtgtgc	acagtaaacg	tgtttgtggg	caacagaaaa	aaaaaaaaaa	aaaaaaaaaa	1752
293	aaaaaaaaaa	aaaaaaaaaa	aaaaaaa				1779

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; N Pos. 7,8,9

Seq#:32; Xaa Pos. 3